RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: _10/660,499_

Source: _IFWO_

Date Processed by STIC: _2/24/04_

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

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FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 703-308-4212; FAX: 703-308-4221

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TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE <u>CHECKER VERSION 4.1 PROGRAM</u>, ACCESSIBLE THROUGH THE U.S PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS.

http://www.uspto.gov/web/offices/pac/checker/chkr41note.htm

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail. Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom. Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses.

1. EFS-Bio (**<http://www.uspto.gov/ebc/efs/downloads/documents.htm>** , EFS Submission User Manual - cPAVE)

2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450

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    U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two. 2011 South Clark Place, Arlington, VA 22202

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Revised 10/08/03

IFWO

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/660,499

DATE: 02/24/2004
TIME: 09:43:29

Input Set : A:\PTO.YF.txt
Output Set: N:\CRF4\02242004\J660499.raw

```
 3 <110> APPLICANT: Seoul National University Industry Foundation
 5 <120> TITLE OF INVENTION: ROOT-SPECIFIC EXPASIN GENE REGULATING ROOT GROWTH
 6        AND OBSTACLE-TOUCHING STRESS RESISTANCE IN THE PLANT
 8 <130> FILE REFERENCE: 20020-02USA
10 <140> CURRENT APPLICATION NUMBER: US 10/660,499
11 <141> CURRENT FILING DATE: 2003-09-12
13 <150> PRIOR APPLICATION NUMBER: KR 2003-19069
14 <151> PRIOR FILING DATE: 2003-03-27
16 <160> NUMBER OF SEQ ID NOS: 9
18 <170> SOFTWARE: KopatentIn 1.71
```

ERRORED SEQUENCES

```
225 <210> SEQ ID NO: 9
226 <211> LENGTH: 29
227 <212> TYPE: DNA
228 <213> ORGANISM: Artificial Sequence
230 <220> FEATURE:
231 <223> OTHER INFORMATION: Primer
234 <400> SEQUENCE: 9
235 agcaagcttg gagttgatgg gaataatca                                          29
E--> 239 (1)  delete
```

pp 1-4

Does Not Comply
Corrected Diskette Needed

see pp 2-3 for more errors

<400>   1

gcacgagctt caacctctca tcattaggca ttcagcaagc aagaaaaaaa a   51

one space only

atg ggc aaa atc atg ctt gtt ttg ggt agc ctc att gga tta tgc tgt   99
Met Gly Lys Ile Met Leu Val Leu Gly Ser Leu Ile Gly Leu Cys Cys
 1 *One space* 5   10   *one space*   15

ttc aca atc act acc tat gcc ttc tca cct tct gga tgg acc aac gcc   147
Phe Thr Ile Thr Thr Tyr Ala Phe Ser Pro Ser Gly Trp Thr Asn Ala
          20   25   30

sample of invalid amino acid placement

in Sequence 1.

Per 1.822 of Sequence Rules, insert only one space

between codons and amino acids; also, place amino acid

directly under its codon

```
<210>    3
<211>    44
<212>    DNA
<213>    Artificial Sequence

<220>
<223>    Primer
```

see p. 4 for error explanation

```
<400>    3
nnggatccga ygcntcnggn acnatgggyg gygctgygyt angg                44
```

```
<210>    4
<211>    37
<212>    DNA
<213>    Artificial Sequence

<220>
<223>    Primer
```

see p.4

```
<400>    4
nnggatcctt kswytgccar ttnnsncccc arttnck                        37
```

```
<210>    5
<211>    519
<212>    DNA
<213>    Artificial Sequence

<220>
<223>    Probe
```

see p.4

```
<400>    5
gaygcnwsng gnacnatggg nggngcntgy ggntayggna ayytntaygc nacnggntay    60
ggnacnmgna cngcngcnyt nwsnacngcn ytnttyaayg ayggngcnws ntgyggncar   120
tgytayaara thathtgyga ytayaarwsn gaywsnmcnt ggtgyathaa rgcnmgnwsn   180
gtnacngtna cngcnacnaa yttytgyccn ccnaayttyg cnytnccnaa yaayaayggn   240
ggntggtgya ayccnccnyt naarcaytty gayatggcnc arccngcntg ggaraarath   300
ggnathtaym gngcngcnat hgtnccngtn ytnttycarm cngtnccntg yaaraarcay   360
ggngcnytnm gnttywsngt naayggnmgn gaytayttyg arytngtnyt nathwsnaay   420
gtnggcnggng cnggnwsnat hcarwsngtn ttyathaarg cnwsnaarac nggntggatg   480
gcnatgwsnm gnaaytgggg nwsnaaytgg carwsnaay                         519
```

Input Set : A:\PTO.YF.txt
Output Set: N:\CRF4\02242004\J660499.raw

error explanation

Use of n's or Xaa's(NEW RULES):
Use of n's and/or Xaa's have been detected in the Sequence Listing.
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
in <220> to <223> section, please explain location of n or Xaa, and which
residue n or Xaa represents.

Seq#:3; N Pos. 1,2,14,17,20,23,42
Seq#:4; N Pos. 1,2,23,24,26,35
Seq#:5; N Pos. 6,9,12,15,21,24,27,33,39,45,51,54,57,63,66,69,72,75,78,81,84
Seq#:5; N Pos. 87,90,93,105,108,111,117,150,156,159,174,177,180,183,186,189
Seq#:5; N Pos. 192,195,198,210,213,222,225,228,240,243,255,258,261,279,285
Seq#:5; N Pos. 288,303,312,315,318,324,327,330,333,342,345,348,363,366,369
Seq#:5; N Pos. 372,378,381,387,390,405,408,411,417,423,426,429,432,435,438
Seq#:5; N Pos. 447,450,462,465,471,474,483,489,492,501,504,516

Input Set : **A:\PTO.YF.txt**
Output Set: **N:\CRF4\02242004\J660499.raw**

```
L:36 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:39 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:42 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:45 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:48 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:51 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:54 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:57 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:60 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:63 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:66 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:72 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:75 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:78 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:139 M:258 W: Mandatory Feature missing, <221> Tag not found for SEQ ID#:3
L:139 M:258 W: Mandatory Feature missing, <222> Tag not found for SEQ ID#:3
L:139 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:0
L:152 M:258 W: Mandatory Feature missing, <221> Tag not found for SEQ ID#:4
L:152 M:258 W: Mandatory Feature missing, <222> Tag not found for SEQ ID#:4
L:152 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4 after pos.:0
L:165 M:258 W: Mandatory Feature missing, <221> Tag not found for SEQ ID#:5
L:165 M:258 W: Mandatory Feature missing, <222> Tag not found for SEQ ID#:5
L:165 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:0
M:341 Repeated in SeqNo=5
L:239 M:254 E: No. of Bases conflict, this line has no nucleotides.
```